

REMARKS

Claims 1-7, 12, 31 and 44-46 are pending. Claims 1, 4, 31 and 44 have been amended. Claims 8-11, 13-30 and 32-43 have been canceled. No new matter has been added.

Rejection of Claims 1-7, 12, 31 and 44-46 Under 35 U.S.C. §101

Claims 1-7, 12, 31 and 44-46 are rejected under 35 U.S.C. §101 “because the invention is not supported by a credible substantial, specific or well established utility.” According to the Examiner,

the art acknowledges that function cannot be predicted based solely on structural similarity of a known protein, and proteins of a same family, sharing a high degree of sequence similarity, may have diverse, and sometimes even opposite biological activities and functions. ... The present specification does not disclose any functional property or biological significance that is directly associated with human TANGO405, and further research to identify such is required, which renders the invention not substantial.

Applicants respectfully traverse this rejection. Contrary to the Examiner’s assertions, the Applicant has provided sufficient evidence to establish that human TANGO 405 is a lectin ortholog of dectin-2 and has similar biological activity to dectin-2. In fact, the information provided in the present application regarding TANGO405 is very similar to that provided in Example 10 of the USPTO Training Material for the Revised Interim Utility Guidelines (hereafter referred to as the “Training Materials”) in which it was found that a “well established utility” was given. Applicants provide the following chart that compares the information provided in Example 10 of the Training Materials to that provided for the claimed invention.

Example 10	TANGO405
1) cDNA library was prepared from human kidney epithelial cells	1) cDNA library was prepared from a mixed lymphocyte reaction
2) The specification discloses ...that SEQ ID NO:2 has a high level of homology to a DNA ligase	2) The present application teaches that TANGO405 has 89% sequence homology with dectin-2
3) The specification teaches that this complete	3) The present application teaches the complete

ORF (SEQ ID NO:2) encodes SEQ ID NO:3	ORF (SEQ ID NO:52) of human TANGO405
4) Alignment of SEQ ID NO:3 with known amino acid sequences of DNA ligases indicates there is a high level of sequence conservation between various known ligases	4) A BLAST of the amino acid sequence of TANGO405 (Exhibit A) indicates that TANGO405 has a high level of homology with many known C-type lectin family members (including dectin-2 and isoforms thereof) and not with other non-C-type lectin family members
5) A search of prior art confirms that ...the next highest level of homology is alpha lectin. However, the latter homology is only 50%	5) A BLAST of the amino acid sequence of TANGO405 (Exhibit A) shows that the next highest level of homology with a non-C-type lectin protein is with an Fc-epsilon receptor III, with a homology of only 35.8%.
6) The overall <i>sequence similarity</i> between SEQ ID NO:3 and the consensus sequence of the known DNA ligases... reveals a similarity score of 95% (emphasis added)	6) The overall <i>sequence identity</i> between dectin-2 and TANGO405 is 89%. In addition, TANGO405 shows high levels <i>sequence similarity</i> with other C-type lectin family members (e.g., 76% <i>sequence similarity</i> with C-type lectin superfamily member 10)
	7) Both dectin-2 and TANGO405 include a single C-type lectin domain at the COOH terminus (which share a high level of sequence identity)
	8) TANGO405 contains C-type lectin domain signature
	9) A frameshift in the murine TANGO405 sequence results in the sequence of dectin-2

Thus, Applicants have provided more information regarding human TANGO405 than what was needed to demonstrate a credible substantial, specific or well established utility according to Example 10 of the Training Materials. The data in the present application provides sufficient evidence to establish that human TANGO 405 is a human ortholog of dectin-2 having similar biological activity.

Furthermore, as noted above, both human TANGO 405 and dectin-2 have a single C-type lectin domain in the COOH terminus. As shown in figure 4, the C-type lectin domain of human TANGO 405 is about 73% identical to the C-type lectin domain of dectin-2. This is a significantly higher level of identity within the C-type lectin domain of dectin-2 than seen with

other C-type lectins. See, e.g., Ariizumi et al. (2000) J. Biol. Chem. 275(16):11957-11963, page 11959 which provides that “the CRD domain in the dectin-2 polypeptide exhibited marked homology with the CRD sequences in other C-type lectins, such as DCIR (44.7%), MGL (43.8%), HL2 (45.8%)” In addition, the COOH-terminal region of both dectin-2 and human TANGO 405 contain all thirteen invariant amino acid residues conserved in the C-type lectin domain of many C-lectins. These high levels of sequence identity in a conserved relevant domain of dectin-2 provides further evidence that murine dectin-2 and human TANGO 405 have similar biological function.

In view of the above, it is clear that Applicants have provided sufficient data to establish a substantial credible utility for the claimed nucleic acid molecules. Therefore, Applicants respectfully request that the Examiner withdraw this rejection.

Rejection of Claims 1-7, 12, 31 and 44-46 Under 35 U.S.C. §112, first paragraph

Claims 1-7, 12, 31 and 44-46 are rejected under 35 U.S.C. §112, first paragraph. Specifically, the Examiner has maintained the argument that “since the claimed invention is not supported by either a credible asserted utility or a well established utility for the reasons set forth above, one skilled in the art would not know how to use the claimed invention.”

Applicants respectfully traverse this rejection. As discussed above in response to the utility rejection, the claimed invention does have a credible asserted utility, and as such one of skill in the art would be able to make and use the claimed invention.

The Examiner further asserts that even though “human TANGO405 and mouse dectin-2 may not share 40 nucleic acids or 15 amino acids with 100% sequence identity, ... there is no way to predict whether the human TANGO405 may share sequence identity with other unknown proteins having a distinct functional property.” Further, the Examiner states that “it is well known in the art that it does not take 100% sequence identity for two molecule to hybridize, and therefore, without specifying regions specific for the human TANGO405 polynucleotide, a

randomly selected fragment of nucleotides from human TANGO405 polypeptide are likely to bind other molecules such as that encoding dectin-2.”

Applicants respectfully traverse this rejection. Several of the claims recite that nucleic acid molecules include at least 40 consecutive nucleic acid residues of the recited sequence or encode a fragment of a polypeptide having at least 15 consecutive amino acids of the recited sequences. Nucleic acid molecules of these lengths are specific to human TANGO 405, as compared to, e.g., dectin-2. As pointed out previously, under certain stringency conditions, probes and primers comprising the claimed nucleic acid fragments would hybridize only to human TANGO 405 polynucleotides. The Examiner seems to be requiring that the probes or primers hybridize under any conditions to only TANGO405. This is not required for the claimed nucleic acid fragments to be useful. Under certain high stringency conditions, nucleic acid fragments of the recited lengths are specific to TANGO405. Moreover, the Examiner has provided absolutely no evidence that the recited nucleic acid fragments would bind other “unknown proteins”. The Examiner appears to be speculating that somewhere out there, there may be a protein-yet to be discovered-that could be encoded by a nucleic acid having at least 40 consecutive residues of the recited nucleic acid sequence

Applicants also note that claim 2 recites a nucleic acid molecule that encodes at least the open reading frame of TANGO405. Claim 45 recites a nucleic acid molecule that includes at least 600 consecutive residues of sequence encoding TANGO405, or that encodes a polypeptide having at least 200 consecutive residues of TANGO405. Nucleic acids of these lengths are clearly specific to human TANGO405.

For the reasons discussed above, Applicants respectfully request that the Examiner withdraw this rejection.

Rejection of Claims 4 and 44 Under 35 U.S.C. §112, second paragraph

Claims 4 and 44 are rejected under 35 U.S.C. §112, second paragraph, “as being indefinite for failing to particularly point out and distinctly claim the subject matter which the

applicant regards as the invention.” In particular, the Examiner states that “claim 4 remains indefinite because … it is unclear what the structural relationship of the heterologous polypeptide with said polypeptide, and whether the two nucleic acids are encoding a fusion protein or two separate proteins.”

Applicants respectfully traverse this rejection. Claim 4 is directed to a nucleic acid that includes a sequence encoding TANGO405 or a portion thereof and a sequence encoding a heterologous protein, i.e., a non-TANGO405 protein. The claim recites one nucleic acid molecule that includes both sequences. Thus, the structural relationship of the two nucleic acid sequences, one encoding TANGO405 and the other encoding a non-TANGO405 protein, is clear. They are contained within the same nucleic acid molecule. Whether the polypeptides encoded by the two sequences are fused or expressed as two separate proteins is not relevant, as the claim is directed to a nucleic acid, and the relationship of the elements of the nucleic acid are clear. Therefore, Applicants respectfully request that the Examiner withdraw this rejection.

With regard to claim 44, the Examiner asserts that “it is unclear what ‘a polypeptide’ is meant, and the host may produce polypeptides other than the polypeptides encoded by the transformed or transfected expression vector.”

Claim 44 has been amended to recite “a polypeptide encoded by a nucleic acid of claim 1”, thereby obviating this rejection.

Applicant : McCarthy et al.
Serial No. : 09/766,511
Filed : January 19, 2001
Page : 11 of 11

Attorney's Docket No.: 10448-209001 / MPI00-
537OMNI

Enclosed is a check for the Petition for Extension of Time fee. Please apply any other charges or credits to deposit account 06-1050.

Respectfully submitted,

Date: 3/23/04



Laurie Butler Lawrence
Reg. No. 46,593

Fish & Richardson P.C.
225 Franklin Street
Boston, MA 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

20818389.doc



Exhibit A

results of BLAST

BLASTP 2.2.7 [Jan-02-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1075243340-3602-98206073622.BLASTQ3

Query=

(209 letters)

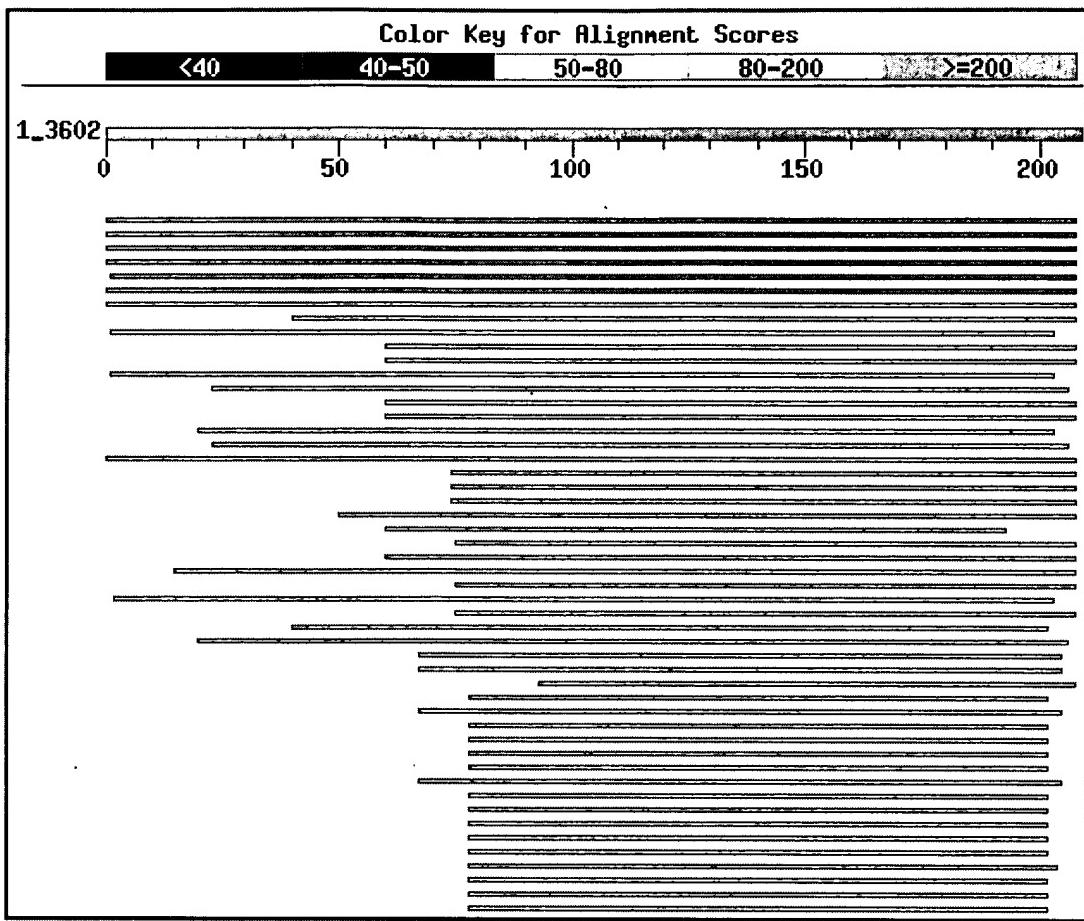
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
1,612,710 sequences; 530,365,172 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Related Structures

		Score (bits)	E Value
Sequences producing significant alignments:			
gi 9910158 ref NP_064385.1	C-type (calcium dependent, carb...	276	2e-73
gi 37181558 gb AAQ88590.1	CLECSF11 [Homo sapiens]	224	8e-58
gi 18466806 ref NP_569708.1	C-type (calcium dependent, car...	223	2e-57
gi 7677472 gb AAF67178.1	dectin-2 beta isoform [Mus musculus]	220	1e-56
gi 38085039 ref XP_355810.1	similar to dendritic cell immu...	209	3e-53
gi 31978955 gb AAP58453.1	dendritic cell immuno-activating...	202	3e-51
gi 7677475 gb AAF67179.1	dectin-2 gamma isoform [Mus muscu...	198	5e-50
gi 17225339 gb AAL37359.1	dendritic lectin b isoform [Homo...	191	8e-48
gi 31542313 ref NP_525126.2	C-type lectin, superfamily mem...	160	1e-38
gi 25392205 pir JC7608	type II lectin-like immunoreceptor ...	160	1e-38
gi 7705338 ref NP_057268.1	C-type lectin, superfamily memb...	160	2e-38
gi 17226268 gb AAL37713.1	C-type lectin-like receptor CLEC...	159	3e-38
gi 26354554 dbj BAC40905.1	unnamed protein product [Mus mu...	159	3e-38
gi 8489015 gb AAF75560.1	HDCGC13P [Homo sapiens]	158	5e-38
gi 37577115 ref NP_919429.1	C-type lectin, superfamily mem...	157	8e-38
gi 34858421 ref XP_342754.1	similar to C-type lectin [Ratt...	157	1e-37
gi 6754728 ref NP_034949.1	C-type lectin, superfamily memb...	156	2e-37
gi 11493654 gb AAG35593.1	C-type lectin DDB27 short form [...	155	5e-37

gi 13386214 ref NP_081494.1	RIKEN cDNA 1810046I24; DCAR al...	155	6e-37	L
gi 37577119 ref NP_919432.1	C-type lectin, superfamily mem...	154	7e-37	L
gi 37577117 ref NP_919430.1	C-type lectin, superfamily mem...	152	4e-36	L
gi 13879298 gb AAH06623.1	Clecsf6 protein [Mus musculus]	151	6e-36	L
gi 18028293 gb AAL56016.1	Fc-epsilon receptor III [Homo sa...	148	7e-35	L
gi 23397421 ref NP_694877.1	RIKEN cDNA 3110037K17 [Mus mus...	147	1e-34	L
gi 6753442 ref NP_036129.1	C-type (calcium dependent, carb...	147	1e-34	L
gi 25050261 ref XP_194289.1	similar to C-type lectin, supe...	142	3e-33	L
gi 26387827 dbj BAC25626.1	unnamed protein product [Mus mu...	142	4e-33	L
gi 7657333 ref NP_055173.1	C-type lectin, superfamily memb...	140	2e-32	L
gi 34858417 ref XP_342753.1	similar to RIKEN cDNA 3110037K...	140	2e-32	L
gi 34858419 ref XP_232393.2	similar to dendritic cell immu...	137	1e-31	L
gi 9910162 ref NP_064332.1	C-type lectin, superfamily memb...	129	4e-29	L
gi 25392184 pir JC7595	scavenger receptor with C-type lect...	96	5e-19	L
gi 38174510 gb AAH60789.1	Collectin sub-family member 12, ...	96	5e-19	L
gi 34858415 ref XP_342752.1	similar to C-type (calcium dep...	96	6e-19	L
gi 27356791 gb AAL89528.1	putative CD209L1 protein [Hyloba...	95	8e-19	
gi 18641360 ref NP_569057.1	collectin sub-family member 12...	95	8e-19	L
gi 27356800 gb AAL89529.1	putative CD209L1 protein [Hyloba...	95	9e-19	
gi 27356809 gb AAL89530.1	putative CD209L1 protein [Hyloba...	95	1e-18	
gi 12084795 gb AAG13815.2	probable mannose binding C-type ...	94	2e-18	L
gi 20149606 ref NP_055072.2	CD209 antigen-like; putative t...	93	3e-18	L
gi 19584340 emb CAD28466.1	hypothetical protein [Homo sapi...	92	4e-18	L
gi 27356856 gb AAL89536.1	putative CD209L1 protein [Pan tr...	92	6e-18	
gi 15383614 gb AAK91863.1	sDC-SIGN2 type I isoform [Homo s...	91	9e-18	L
gi 18157520 dbj BAB83835.1	supported by GENSCAN and partia...	91	9e-18	
gi 27356845 gb AAL89534.1	putative CD209L1 protein [Gorill...	91	9e-18	
gi 34870124 ref XP_344065.1	similar to SIGNR3 [Rattus norv...	91	1e-17	L
gi 27356883 gb AAL89539.1	putative CD209 protein [Hylobate...	91	2e-17	
gi 27356854 gb AAL89535.1	putative CD209L1 protein [Pan tr...	91	2e-17	
gi 12084797 gb AAG13848.2	probable mannose binding C-type ...	90	2e-17	L
gi 27356874 gb AAL89538.1	putative CD209 protein [Hylobate...	89	4e-17	
gi 15383618 gb AAK91865.1	sDC-SIGN2 type III isoform [Homo...	89	4e-17	L
gi 27356910 gb AAL89542.1	putative CD209 protein [Pongo py...	89	5e-17	
gi 27356901 gb AAL89541.1	putative CD209 protein [Pongo py...	89	6e-17	
gi 6680734 ref NP_031519.1	asialoglycoprotein receptor 2 [...	89	7e-17	L
gi 27356928 gb AAL89544.1	putative CD209 protein [Pan trog...	89	7e-17	
gi 34877879 ref XP_341575.1	similar to collectin placenta ...	88	8e-17	L
gi 27356892 gb AAL89540.1	putative CD209 protein [Hylobate...	88	9e-17	
gi 16118455 gb AAL14428.1	dendritic cell-specific ICAM-3 g...	88	1e-16	
gi 16118475 gb AAL14438.1	dendritic cell-specific ICAM-3 g...	88	1e-16	
gi 18652791 gb AAK74185.1	type II membrane protein CD209 [...	88	1e-16	
gi 15420784 gb AAK97459.1	dendritic cell-specific ICAM-3 g...	88	1e-16	
gi 15420782 gb AAK97458.1	dendritic cell-specific ICAM-3 g...	88	1e-16	
gi 37779180 gb AAP03436.1	dendritic cell-specific ICAM-3 g...	87	1e-16	
gi 23498707 emb CAD28398.1	putative mannose-binding C-type...	87	1e-16	
gi 10863957 ref NP_066978.1	CD209 antigen; dendritic cell-...	87	1e-16	L
gi 27356865 gb AAL89537.1	putative CD209 protein [Papio ha...	87	1e-16	
gi 27356919 gb AAL89543.1	putative CD209 protein [Gorilla ...	87	1e-16	
gi 15281089 gb AAK91854.1	mDC-SIGN1B type I isoform [Homo ...	87	2e-16	L
gi 27356930 gb AAL89545.1	putative CD209 protein [Pan trog...	87	2e-16	

gi 4502253 ref NP_001172.1	asialoglycoprotein receptor 2 i...	87	2e-16	L
gi 15281081 gb AAK91850.1	sDC-SIGN1A type I isoform [Homo ...	87	3e-16	L
gi 33328316 gb AAQ09608.1	HBxAg-binding protein [Homo sapi...	87	3e-16	L
gi 34870060 ref XP_341024.1	similar to CD209 antigen; dend...	87	3e-16	L
gi 15281077 gb AAK91848.1	mDC-SIGN1A type III isoform [Hom...	86	3e-16	L
gi 15281091 gb AAK91855.1	sDC-SIGN1B type I isoform [Homo ...	86	4e-16	L
gi 23498708 emb CAD28399.1	putative mannose-binding C-type...	86	4e-16	
gi 15281083 gb AAK91851.1	sDC-SIGN1A TYPE II isoform [Homo...	86	4e-16	L
gi 22651471 gb AAL71882.1	C-type lectin CD209L2 [Macaca mu...	86	5e-16	
gi 18426877 ref NP_550436.1	asialoglycoprotein receptor 2 ...	86	6e-16	L
gi 8392926 ref NP_058885.1	asialoglycoprotein receptor 2; ...	86	6e-16	L
gi 18426875 ref NP_550435.1	asialoglycoprotein receptor 2 ...	85	7e-16	L
gi 33667103 ref NP_878910.1	C-type lectin, superfamily mem...	85	7e-16	L
gi 5453684 ref NP_006335.1	C-type (calcium dependent, carb...	85	7e-16	L
gi 206649 gb AAA42038.1	asialoglycoprotein receptor (RHL2)	85	7e-16	L
gi 16758588 ref NP_446205.1	C-type lectin, superfamily mem...	85	8e-16	L
gi 18777736 ref NP_570974.1	CD209d antigen [Mus musculus] ...	85	9e-16	L
gi 15281093 gb AAK91856.1	sDC-SIGN1B type II isoform [Homo...	85	9e-16	L
gi 126136 sp P08290 LECI_RAT	Asialoglycoprotein receptor R2...	85	1e-15	
gi 15928688 gb AAH14811.1	Macrophage galactose N-acetyl-ga...	84	1e-15	L
gi 17017253 gb AAL33584.1	SIGNR3 [Mus musculus]	84	1e-15	L
gi 6754688 ref NP_034926.1	macrophage galactose N-acetyl-g...	84	1e-15	L
gi 26335321 dbj BAC31361.1	unnamed protein product [Mus mu...	84	1e-15	
gi 21901969 dbj BAC05523.1	collectin placenta 1 [Mus muscu...	84	1e-15	L
gi 15281085 gb AAK91852.1	sDC-SIGN1A type III isoform [Hom...	84	2e-15	L
gi 18158893 pdb 1K9J A	Chain A, Complex Of Dc-Signr And Glc...	83	3e-15	S
gi 18485494 ref NP_569716.1	collectin sub-family member 12...	83	4e-15	L
gi 34870118 ref XP_221808.2	similar to DC-SIGN [Rattus nor...	82	4e-15	L

Alignments

 Get selected sequences Select all Deselect all

>gi|9910158|ref|NP_064385.1| L C-type (calcium dependent, carbohydrate recognition superfamily member 10 [Mus musculus]

gi|7677469|gb|AAF67177.1| L lectin-2 alpha isoform [Mus musculus]

gi|18606438|gb|AAH23008.1| L C-type (calcium dependent, carbohydrate recognition superfamily member 10 [Mus musculus]

Length = 209

Score = 276 bits (706), Expect = 2e-73

Identities = 144/211 (68%), Positives = 162/211 (76%), Gaps = 4/211 (1%)

Query: 1 MMQEQQPQSTEKRGLSLRLWSVAGISIALLSACFIVSCVVVTYHFTYGETGKRLSELHSY 60
M+QE+Q Q K +LRLWS A IS+ LLS CFI SCVVVTY F + +RL ELH+Y

Sbjct: 1 MVQERQSQG--KGVCWTLRLWSAAVISMLLLSTCFIASCVVTYQFIMDQPSRRLYELHTY 58

Query: 61 HSSLTCFSEGTKVPA--WGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFN 118

HSSLTCFSEGT V WGCCP WKSFGSSCY IS++E WS SEQNCV+MGAHLVV N
 Sbjct: 59 HSSLTCFSEGTMVSEKMWGCCPNHWKSFGSSCYLISTKENFWSTSEQNCVQMG AHLVVIN 118

Query: 119 TEAEQNFI VQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
 TEAEQNFI QQLNES SYFLGLSDPQGN WQWID TP+ +NVRFWH EPN E+C S
 Sbjct: 119 TEAEQNFI TQQLNESLSYFLGLSDPQGNKGWQWIDDTPFSQNVRFWHPHEPNLPEERCVS 178

Query: 179 IVFWKPTGWGWNNDVICETRRNSICEMNKIYL 209
 IV+W P+ WGWNDV C++ NSICEM KIYL
 Sbjct: 179 IVYWNPSKWGWNDVFCDSKHNSICEMKKIYL 209

[>] >gi|37181558|gb|AAQ88590.1| CLECSF11 [Homo sapiens]
 Length = 213

Score = 224 bits (571), Expect = 8e-58
 Identities = 116/213 (54%), Positives = 146/213 (68%), Gaps = 4/213 (1%)

Query: 1 MMQEQQPQSTEK-RGWLSLRWVAGISIALLSACFIVSCVVTYHFTYGETGKRLSEL-- 57
 M+ E++PQ EK W L++WS+A +SI LLS CF VS VV +F Y +T KRLS+L
 Sbjct: 1 MVPEEEPDREKGLWWFQLKVWSMAVVSILL SVCFTVSSVPHNFMSKTVKRLSKLRE 60

Query: 58 -HSYHSSLTCFSEGTKVPAGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVV 116
 YHSSLTC EG + W CCP W SF SSCYFIS+ + W+KS++NC MGA LVV
 Sbjct: 61 YQQYHSSLTCVMEGKDIEDWSCCPTPWTSFQSSCYFISTGMQSWTKSQKNCSVGMADLVV 120

Query: 117 FNTEAEQNFI VQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQC 176
 NT EQ+FI+Q L + SYFLGLSDP G +WQW+D+TPY +NV FWH GEPN+ E+C
 Sbjct: 121 INTREEQDFIIQNLKRNSSYFLGLSDPGGRRHWQVDQTPYNENVTFWHSGEPNLDERC 180

Query: 177 ASIVFWKPTGWGWNNDVICETRRNSICEMNKIYL 209
 A I F WGWND+ C + SIC+M KIY+
 Sbjct: 181 AIINFRSSEEWGWNDIHCHVPQKSICKMKKIYI 213

[>] >gi|18466806|ref|NP_569708.1| [L] C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 11; dendritic cell lectin b; blood dendritic cell antigen 2 protein; C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 7 [Homo sapiens]

gi|17224598|gb|AAL37036.1| [L] blood dendritic cell antigen 2 protein [Homo sapiens]

gi|17225337|gb|AAL37358.1| [L] dendritic lectin [Homo sapiens]
 Length = 213

Score = 223 bits (568), Expect = 2e-57
 Identities = 115/213 (53%) Positives = 145/213 (68%), Gaps = 4/213 (1%)

Query: 1 MMQEQQPQSTEK-RGWLSLRWVAGISIALLSACFIVSCVVTYHFTYGETGKRLSEL-- 57
 M+ E++PQ EK W L++WS+A +SI LLS CF VS VV +F Y +T KRLS+L
 Sbjct: 1 MVPEEEPDREKGLWWFQLKVWSMAVVSILL SVCFTVSSVPHNFMSKTVKRLSKLRE 60

Query: 58 -HSYHSSLTCFSEGTKVPAGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVV 116
 YH SLTC EG + W CCP W SF SSCYFIS+ + W+KS++NC MGA LVV
 Sbjct: 61 YQQYHSSLTCVMEGKDIEDWSCCPTPWTSFQSSCYFISTGMQSWTKSQKNCSVGMADLVV 120

Query: 117 FNTEAEQNFI VQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQC 176
 NT EQ+FI+Q L + SYFLGLSDP G +WQW+D+TPY +NV FWH GEPN+ E+C

Sbjct: 121 INTREEQDFIIQNLKRNSSYFLGLSDPGGRRHWQWVDQTPYNENVTFWHSGEPNNLDERC 180

Query: 177 ASIVFWKPTGWGWNDVICETRRNSICEMNKIYL 209

A I F WGWND+ C + SIC+M KIY+

Sbjct: 181 AIINFRSSEEWGWNDIHCHVPQKSICKMKKIYL 213

[>] >gi|7677472|gb|AAF67178.1| [L] lectin-2 beta isoform [Mus musculus]
Length = 175

Score = 220 bits (560), Expect = 1e-56

Identities = 122/209 (58%), Positives = 137/209 (65%), Gaps = 34/209 (16%)

Query: 1 MMQEQQPQSTEKRGWLSSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSY 60
M+QE+Q Q K +LRLWS A IS+ LLS CFI SCV

Sbjct: 1 MVQERQSQG--KGVCWTLRLWSAAVISMLLLSTCFIASCVEK----- 40

Query: 61 HSSLTCFSEGTVPAWGCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTE 120
WGCP WKSFGSSCY IS++E WS SEQNCV+MGAHLVV NTE

Sbjct: 41 -----MWGCCPNHWKSFGSSCYLISTKENFWSTSEQNCVQMGAHLVVINTE 86

Query: 121 AEQNFIIVQQLNESFSYFLGLSDPQGNWWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIV 180
AEQNFI IQLNES SYFLGLSDPQGN WQWID TP+ +NVRFWH EPN E+C SIV

Sbjct: 87 AEQNFIITQQLNESLSYFLGLSDPQGNNGKWQWIDDTPSQNVRFWHPHEPNLPEERCIVSIV 146

Query: 181 FWKPTGWGWNDVICETRRNSICEMNKIYL 209

+W P+ WGWNDV C+++ NSICEM KIYL

Sbjct: 147 YWNPSKKGWNDVFCDSKHNSICEMKKIYL 175

[>] >gi|38085039|ref|XP_355810.1| [L] similar to dendritic cell immuno-activating receptor alpha isoform [Mus musculus]
Length = 208

Score = 209 bits (532), Expect = 3e-53

Identities = 109/211 (51%), Positives = 141/211 (66%), Gaps = 6/211 (2%)

Query: 2 MQEQQPQSTEKRGWLSSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYH 61
M +++P + W SLRLW A ISI LLS CFI SCVVTY + +RLSELH+YH

Sbjct: 1 MMQERPAQQVVCW-SLRLWMAALISILLSTCFIASCVVTYQLMMNKPNRRLSELHTYH 59

Query: 62 SSLTCFSEGTVPAWGCPASWKSFGSSCYFISSEEKV-WSKSEQNCVEMGAHLVVFN 118
S+L CFSEGTVPAWGCPASWKSFGSSCYFISSEEKV-WSKSEQNCVEMGAHLVVFN 118

Sbjct: 60 SNLICFSEGTTVSEKVVSCCPKDWPFGSYCYFTSTDASQNKSEEKCSLRGAHLVVIH 119

Query: 119 TEAEQNFIIVQQLNESFSYFLGLSDPQGNWWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178

++ EQ+FI + L+ + YF+GLSD GN+ W+WID+TPY FWH GEPN+ E+C

Sbjct: 120 SQEEQDFITRMLDTAAGYFIGLSD-VGNSQWRWIDQTPYNDRATFWHKGEPPNDYEKCV- 177

Query: 179 IVFWKPTGWGWNDVICETRRNSICEMNKIYL 209

I+ ++ T WGWND+ C NS+C+M KIYL

Sbjct: 178 ILNYRKTMWGWNDIDCSDEENSVCQMKKIYL 208

[>] >gi|31978955|gb|AAP58453.1| dendritic cell immuno-activating receptor alpha isoform [Mus musculus]

Length = 209

Score = 202 bits (514), Expect = 3e-51
 Identities = 110/213 (51%), Positives = 143/213 (67%), Gaps = 8/213 (3%)

Query: 1 MMQEQQPQSTEKRGWLSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSY 60
 M+QE+Q Q + W SLRLWS A ISI LLS CFI SCVVTY F+ + +RLSEL Y
 Sbjct: 1 MVQERQLQG-KAVSW-SLRLWSAAVISILLSTCFIASCVVTYQFSMDKPNRRLSELDRY 58

Query: 61 HSSLTCFSEGTKVP--AWGCCPASWKSFGSSCYFISS--EEKVWSKSEQNCVEMGAHLVV 116
 HS LTCFSEG V W CCP WK FGS CY + + W+KSE+NC MGAHLVV
 Sbjct: 59 HS-LTCFSEGNMVSDFKVVSCCPKDWLKGSHCYLVPTVFSSASWNKSEENCSRMGAHLVV 117

Query: 117 FNTEAEQNFI VQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQC 176
 +++ EQ+FI L+ +YF+GL D G+ WQW+D+TPYE++V FWH GEP+ E+C
 Sbjct: 118 IHSQEEQDFITGILDIAAYFIGLWD-TGHRQWQWVDQTPYEESVTFWHNGEPSSDNEKC 176

Query: 177 ASIVFWKPTGWGWNDVICETRRNSICEMNKIYL 209
 ++ + + GWGWND+ C ++ S+C+M KI L
 Sbjct: 177 VTVYYRRNIGWGWNDISCNLKQKSVQCQMKKINL 209

[>] >gi|7677475|gb|AAF67179.1| [L] dectin-2 gamma isoform [Mus musculus]
 Length = 168

Score = 198 bits (504), Expect = 5e-50
 Identities = 117/211 (55%), Positives = 132/211 (62%), Gaps = 45/211 (21%)

Query: 1 MMQEQQPQSTEKRGWLSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSY 60
 M+QE+Q Q K +LRLWS A IS+ LLS CFI SCVVTY F + +RL ELH+Y
 Sbjct: 1 MVQERQSQG-KGVCWTLRLWSAAVISMLLSTCFIASCVVTYQFIMDQPSRRLYELHTY 58

Query: 61 HSSLTCFSEGTKVPA--WGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFN 118
 HSSLTCFSEGT V WGCPP WKSFGSSCY IS+E WS SEQNCV+MGAHLVV N
 Sbjct: 59 HSSLTCFSEGTMVSEKMWGCCPNHWKSFGSSCYLISTKENFWSTSEQNCVOMGAHLVVIN 118

Query: 119 TEAEQNFI VQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
 TEAEQNFI QQLNES SYFLGLS+P
 Sbjct: 119 TEAEQNFI TQQLNESLSYFLGLSNP----- 143

Query: 179 IVFWKPTGWGWNDVICETRRNSICEMNKIYL 209
 + WGWNDV C+++ NSICEM KIYL
 Sbjct: 144 -----SKWGWNDVFCDSKHNSICEMKKIYL 168

[>] >gi|17225339|gb|AAL37359.1| [L] dendritic lectin b isoform [Homo sapiens]
 Length = 182

Score = 191 bits (484), Expect = 8e-48
 Identities = 94/172 (54%), Positives = 117/172 (68%), Gaps = 3/172 (1%)

Query: 41 VTYHFTYGETGKRLSEL---HSYHSSLTCFSEGTKVPAWGCPPASWKSFGSSCYFISSEE 97
 V ++F Y +T KRLS+L YH SLTC EG + W CCP W SF SSCYFIS+
 Sbjct: 11 VPHNFMYSKTVKRLSKLREYQQYHPSLTCVMEGKDIEDWSCCPWTSFQSSCYFISTGM 70

Query: 98 KVWSKSEQNCVEMGAHLVVFNTEAEQNFI VQQLNESFSYFLGLSDPQGNNNWQWIDKTPY 157
 + W+KS++NC MGA LVV NT EQ+FI+Q L + SYFLGLSDP G +WQW+D+TPY

Subjct: 71 QSWTKSQKNCSVMGADLVVINTREEQDFIIQNLKRNSSYFLGLSDPGGRRHWQVDQTPY 130

Query: 158 EKNVRFWHLGEPNHSAEQCASIVFWKPTGWWNDVICETRRNSICEMNKIYL 209
+NV FWH GEPN+ E+CA I F WGWND+ C + SIC+M KIY+

Subjct: 131 NENVTFWHSGEPNLDERCAIINFRSSEEWGWNDIHCHVPQKSICKMKKIYI 182

[>gi|31542313|ref|NP_525126.2| L C-type lectin, superfamily member 8; C-type lect [Homo sapiens]

gi|21595255|gb|AAH32313.1| L C-type lectin, superfamily member 8 [Homo sapiens]
Length = 215

Score = 160 bits (406), Expect = 1e-38
Identities = 84/210 (40%), Positives = 126/210 (60%), Gaps = 8/210 (3%)

Query: 2 MQEQQPQSTEKRGWLSSLRLWSV-AGISIALLSACFIVSCVVTYH-FTYGETGKRLSELHS 59
M ++PQS + G + SV A + I LLS CFI SC+VT+H F+ + G + +L

Subjct: 1 MGLEKPQSKLEGGMHPQLIPSVIAVVFILLSVCFIASCLVTHHNFSRCKRGTGVHKLE- 59

Query: 60 YHSSLTCFSEGKVKPA-----WGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHL 114
+H+ L C E +++ + W CCP W++F S+CYF ++ K W++SE+NC MGAHL

Subjct: 60 HHAKLKCIKEKSELKSAEGSTWNCCPIDWRAFQSNCYFPLTDNKWTWAESERNCSGMGAHL 119

Query: 115 VVFNTAEQNFIHQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAE 174
+ +TEAEQNFI+Q L+ SYFLGL D W+W+D+TP+ FWH EP++S

Subjct: 120 MTISTEAEQNFIHQFLDRRLSYFLGLRDENAKGQWRWVDQTPFNPRRVFWHKNEPDNSQG 179

Query: 175 QCASIVFWKPTGWWNDVICETRRNSICEM 204
+ ++ + W WNDV C + IC++

Subjct: 180 ENCVVLVYNQDKWAWNDVPCNFSEASRICKI 209

[>gi|25392205|pir||JC7608 type II lectin-like immunoreceptor - human

gi|6502535|gb|AAF14348.1| L C-type lectin superfamily 6 [Homo sapiens]
Length = 237

Score = 160 bits (405), Expect = 1e-38
Identities = 77/152 (50%), Positives = 102/152 (67%), Gaps = 3/152 (1%)

Query: 61 HSSLTCFSEGKVK--PAWGCPPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFN 118
H++L C + V AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V N

Subjct: 86 HTTLECVKKNMPVEETAWSCCPKNWKSFSNCYFISTESASWQDSEKDCARMEAHLLVIN 145

Query: 119 TEAEQNFIHQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
T+ EQ+FI Q L E +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C

Subjct: 146 TQEEQDFIFQNLQEESAYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPREPSDPNERCVV 205

Query: 179 IVFWK-PTGWWNDVICETRRNSICEMNKIYL 209
+ F K P WGWNDV C + S+CEM KI+L

Subjct: 206 LNFRKSPKRWGWNDVNCLGPQRSVCEMMKIHL 237

[>gi|7705338|ref|NP_057268.1| L C-type lectin, superfamily member 6 isoform 1; de immunoreceptor; C-type lectin; lectin-like immunoreceptor [Homo sapiens]

gi|5823974|emb|CAB54001.1| [L] dendritic cell immunoreceptor [Homo sapiens]
Length = 237

Score = 160 bits (404), Expect = 2e-38
Identities = 77/152 (50%), Positives = 102/152 (67%), Gaps = 3/152 (1%)

Query: 61 HSSLTCFSEGTKV--PAWGCPPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFN 118
H++L C + V AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V N
Sbjct: 86 HTTLECVKKNMPVEETAWSCCPKNWKSFSNCYFISTESASWQDSEKDCARMEAHLLVIN 145

Query: 119 TEAEQNFIIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
T+ EQ+FI Q L E +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C
Sbjct: 146 TQEEQDFIFQNLQEEESAYFVG LSDPEGQRHWQWDQTPYNESSTFWHPREPSDPNERCVV 205

Query: 179 IVFWK-PTGWGWNNDVICETRRNSICEMNKIYL 209
+ F K P WGNDV C + S+CEM KI+L
Sbjct: 206 LNFRKSPKRWGWNNDVNCLGPQRSVCCEMMKIHL 237

[>gi|17226268|gb|AAL37713.1| [L] C-type lectin-like receptor CLEC-6 [Homo sapiens]
gi|31321980|gb|AAM75389.1| [L] C-type lectin-like receptor 6 [Homo sapiens]
Length = 215

Score = 159 bits (402), Expect = 3e-38
Identities = 83/210 (39%), Positives = 125/210 (59%), Gaps = 8/210 (3%)

Query: 2 MEQQQPQSTEKRGWLSSLRLWSV-AGISIALLSACFIVSCVVTYH-FTYGETGKRLSELHS 59
M ++PQS + G + SV A + I LL CFI SC+VT+H F+ + G + +L
Sbjct: 1 MGLEKPQSKLEGGMHPQLIPSVIAVVFILLGVCFIASCLVTHHNFSRCKRGTVHKLE- 59

Query: 60 YHSSLTCFSEGTKVPA----WGCPPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHL 114
+H+ L C E +++ + W CCP W++F S+CYF ++ K W++SE+NC MGAHL
Sbjct: 60 HHAKLKCIKEKSELKSAEGSTWNCCPIDWRRAFQSNCYFPLTDNKWTAESERNCSGMGAHL 119

Query: 115 VVFNTAEQNFIIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAE 174
+ +TEAEQNFI+Q L+ SYFLGL D W+W+D+TP+ FWH EP++S
Sbjct: 120 MTISTEAEQNFIIQFLDRRLSYFLGLRDENAKGQWRWVDQTPNPRRVFWHKNEPDNSQG 179

Query: 175 QCASIVFWKPTGWGWNNDVICETRRNSICEM 204
+ ++ + W WNDV C + IC++
Sbjct: 180 ENCVVLVYNQDKWAWNDVPCNFEASRICKI 209

[>gi|26354554|dbj|BAC40905.1| unnamed protein product [Mus musculus]
Length = 219

Score = 159 bits (402), Expect = 3e-38
Identities = 81/188 (43%), Positives = 113/188 (60%), Gaps = 4/188 (2%)

Query: 24 AGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSEGTKVPA----WGCC 79
A +SI+ LSACFI +C+VT+H+ T + +L YH+ +TC EG + A W CC
Sbjct: 24 AVVSISFLSACFISTCLVTHHYFLRWTRGSVVKLSDYHTRVTCIREGPQPGATGGTWTCC 83

Query: 80 PASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIIVQQLNESFSYFLG 139
P SW++F S+CYF ++ + W +SE+NC M +HLV NTEAEQNFI+ Q L++ FSYFLG
Sbjct: 84 PVSWRAFQSNCYFPLNDNQTWHESERNCSSGMSSHLVTINTEAEQNFTQLLDKRFSYFLG 143

Query: 140 LSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSSEQCASIVFWKPTGWGWNVICETRRN 199
 L+D WQW+DKTP+ + FW GE N E+ ++ W WND C
 Sbjct: 144 LADENVEGQWQWVDKTPFNPHTVFWEKGESNDFMEEDCVVLVHVHEKWVWNDFPCHFEVR 203
 Query: 200 SICEMNKI 207
 IC++ I
 Sbjct: 204 RICKLPGI 211

[>]gi|8489015|gb|AAF75560.1| L HDCGC13P [Homo sapiens]
 Length = 237

Score = 158 bits (400), Expect = 5e-38
 Identities = 76/152 (50%), Positives = 101/152 (66%), Gaps = 3/152 (1%)

Query: 61 HSSLTCFSEGTKV--PAWGCPPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFN 118
 H++L C + V AW CCP +WKSF S+CYFIS+E W E++C M AHL+V N
 Sbjct: 86 HTTLECVKKNMPVEETAWSCCPKNWKSFSNCYFISTESASWQDCEKDCARMEAHLLVIN 145

Query: 119 TEAEQNFIQQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSSEQCAS 178
 T+ EQ+FI Q L E +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C
 Sbjct: 146 TQEEQDFIFQNLQEEESAYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPREPSDPNERCVV 205

Query: 179 IVFWK-PTGWGWNVICETRRNSICEMNKIYL 209
 + F K P WGWNDV C + S+CEM KI+L
 Sbjct: 206 LNFRKSPKRWGWNDVNCLGPQRSVCEMMKIHL 237

[>]gi|37577115|ref|NP_919429.1| L C-type lectin, superfamily member 6 isoform 3; c
 immunoreceptor; C-type lectin; lectin-like
 immunoreceptor [Homo sapiens]
 Length = 197

Score = 157 bits (398), Expect = 8e-38
 Identities = 77/152 (50%), Positives = 102/152 (67%), Gaps = 3/152 (1%)

Query: 61 HSSLTCFSEGTKV--PAWGCPPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFN 118
 H++L C + V AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V N
 Sbjct: 46 HTTLECVKKNMPVEETAWSCCPKNWKSFSNCYFISTESASWQDSEKDCARMEAHLLVIN 105

Query: 119 TEAEQNFIQQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSSEQCAS 178
 T+ EQ+FI Q L E +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C
 Sbjct: 106 TQEEQDFIFQNLQEEESAYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPREPSDPNERCVV 165

Query: 179 IVFWK-PTGWGWNVICETRRNSICEMNKIYL 209
 + F K P WGWNDV C + S+CEM KI+L
 Sbjct: 166 LNFRKSPKRWGWNDVNCLGPQRSVCEMMKIHL 197

[>]gi|34858421|ref|XP_342754.1| L similar to C-type lectin [Rattus norvegicus]
 Length = 226

Score = 157 bits (397), Expect = 1e-37
 Identities = 83/196 (42%), Positives = 114/196 (58%), Gaps = 13/196 (6%)

Query: 21 WSVAGISIALLSACFIVSCV-----VTYHFTYGETGKRLSELHSYHSSLTCFSE--- 69

W A +SI+ LSACFI +C+ VT++F + G L + YH+ LTC E
 Sbjct: 21 WVCAVVSISFLSACFISTCLGKLLFLLTVTHYFLLWKRGSAK-FSDYHTRLTCILEEPQ 79

Query: 70 -GTKVPAWGCPPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIHQ 128
 G W CCP SW++F S+CYF ++ + W +SE+NC M +HLV NTEAEQ+F+ Q
 Sbjct: 80 PGATGGTWTCCPVSWRQFQSNCFPLNDNQTWHESERNCSGMSSHLLVTINTEAEQDFVTQ 139

Query: 129 QLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSSEQCASIVFWKPTGWG 188
 L+E FSYFLGLS + WQW+DKTP+ NV FW +GEP E+ ++ + W
 Sbjct: 140 LLDEQFSYFLGLSYEKVEGQWQWVDKTPFNPVNFWKVGEPKDYMEECVVLVYDQDKWV 199

Query: 189 WNDVICETRRNSICEM 204
 WND C IC++
 Sbjct: 200 WNDFPCHFEMGRICKL 215

>gi|6754728|ref|NP_034949.1| C-type lectin, superfamily member 8; macrophage C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 [Mus musculus]
gi|4159801|gb|AAD05125.1| C-type lectin [Mus musculus]
 Length = 219

Score = 156 bits (395), Expect = 2e-37
 Identities = 80/188 (42%), Positives = 111/188 (59%), Gaps = 4/188 (2%)

Query: 24 AGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSE---GTKVPAWGCCCC 79
 A +SI+ LSACFI +C+VT+H+ T + +L YH+ +TC E G W CC
 Sbjct: 24 AVVSISFLSACFISTCLVTHHYFLRWTRGSVVKLSDYHTRVTCIREEPQPGATGGTWTCC 83

Query: 80 PASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIHQQLNESFSYFLG 139
 P SW++F S+CYF ++ + W +SE+NC M +HLV NTEAEQNF+ Q L++ FSYFLG
 Sbjct: 84 PVSWRAFQSNCFPLNDNQTWHESERNCSGMSSHLLVTINTEAEQNFVTQLLDKRFSYFLG 143

Query: 140 LSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSSEQCASIVFWKPTGWGNDVICETRRN 199
 L+D WQW+DKTP+ + FW GE N E+ ++ W WND C
 Sbjct: 144 LADENVEGQWQWVDKTPFNPHTVWEKGESNDFMEEDCVVLVHVHEKWVWNDFPCHFEVR 203

Query: 200 SICEMNKI 207
 IC++ I
 Sbjct: 204 RICKLPGI 211

>gi|11493654|gb|AAG35593.1| C-type lectin DDB27 short form [Homo sapiens]
 Length = 204

Score = 155 bits (391), Expect = 5e-37
 Identities = 73/136 (53%), Positives = 95/136 (69%), Gaps = 1/136 (0%)

Query: 75 AWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIHQQLNESF 134
 AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V NT+ EQ+FI Q L E
 Sbjct: 69 AWSCCPKNWKSFSNCYFISTESASWQDSEKDCARMEAHLVINTQEEQDFIFQNLQEES 128

Query: 135 SYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSSEQCASIVFWK-PTGWGNDVI 193
 +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C + F K P WGNDV
 Sbjct: 129 AYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPREPSDPNERCVVLNFRKSPKRWGNDVN 188

Query: 194 CETRRNSICEMNKIYL 209

C + S+CEM KI+L
 Sbjct: 189 CLGPQRSVCEMMKIHL 204

[>] >gi|13386214|ref|NP_081494.1| [L] RIKEN cDNA 1810046I24; DCAR alpha; DCAR beta; deimmunoactivating receptor [Mus musculus]

gi|12841568|dbj|BAB25260.1| [L] unnamed protein product [Mus musculus]

gi|31978957|gb|AAP58454.1| [L] dendritic cell immuno-activating receptor beta isoform [Mus musculus]

Length = 176

Score = 155 bits (391), Expect = 6e-37

Identities = 90/211 (42%), Positives = 120/211 (56%), Gaps = 37/211 (17%)

Query: 1 MMQEQQPQSTEKRGWLSSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSY 60
 M+QE+Q Q + W SLRLWS A ISI LLS CFI SCV

Sbjct: 1 MVQERQLQG-KAVSW-SLRLWSAAVISILLSTCFIASCVDK----- 40

Query: 61 HSSLTCFSEGTKVPAWGCPASWKSFGSSCYFISS--EEKVWSKSEQNCVEMGAHLVVFN 118
 W CCP WK FGS CY + + W+KSE+NC MGAHLVV +

Sbjct: 41 -----VWSCCPKDWKLFGSHCYLVPTVFSSASWNKSEENCSRNGAHLVVIH 86

Query: 119 TEAEQNFIIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
 ++ EQ+FI L+ +YF+GL D G+ WQW+D+TPYE++V FWH GEP+ E+C +

Sbjct: 87 SQEEQDFITGILDIHAAYFIGLWD-TGHRQWQVDQTPYEEESVTFWHNGEPSSDNEKCVT 145

Query: 179 IVFWKPTGWWNDVICETRRNSICEMNKIYL 209
 + + + GWGWND+ C ++ S+C+M KI L

Sbjct: 146 VYYRRNIGWGWNDISCNLKQKSVQCQMKKINL 176

[>] >gi|37577119|ref|NP_919432.1| [L] C-type lectin, superfamily member 6 isoform 2; immunoreceptor; C-type lectin; lectin-like immunoreceptor [Homo sapiens]

Length = 204

Score = 154 bits (390), Expect = 7e-37

Identities = 73/136 (53%), Positives = 95/136 (69%), Gaps = 1/136 (0%)

Query: 75 AWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIIVQQLNESF 134
 AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V NT+ EQ+FI Q L E

Sbjct: 69 AWSCCPKNWKSFSNCYFISTESASWQDSEKDCARMEAHLLVINTQEEQDFIFQNLQEES 128

Query: 135 SYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWK-PTGWWNDVI 193
 +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C + F K P WGWNDV

Sbjct: 129 AYFVGLSDPEGQRHWQWDQTPYNESSTFWHPREPSDPNERCVVLNFRKSPKRWGWNDVN 188

Query: 194 CETRRNSICEMNKIYL 209
 C + S+CEM KI+L

Sbjct: 189 CLGPQRSVCEMMKIHL 204

[>] >gi|37577117|ref|NP_919430.1| [L] C-type lectin, superfamily member 6 isoform 4; immunoreceptor; C-type lectin; lectin-like immunoreceptor [Homo sapiens]

Length = 165

Score = 152 bits (383), Expect = 4e-36
 Identities = 73/136 (53%), Positives = 95/136 (69%), Gaps = 1/136 (0%)

Query: 75 AWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIIVQLNESF 134
 AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V NT+ EQ+FI Q L E
 Sbjct: 30 AWSCCPKNWKSFSNCYFISTESASWQDSEKDCARMEAHLLINTQEEQDFIFQNLQEES 89

Query: 135 SYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSSEQCASIVFWK-PTGWGWNDVI 193
 +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C + F K P WGWNDV
 Sbjct: 90 AYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPREPSDPNERCVVLFNRKSPKRWGWNDVN 149

Query: 194 CETRRNSICEMNKIYL 209
 C + S+CEM KI+L
 Sbjct: 150 CLGPQRSVCEMMKIHL 165

>gi|13879298|gb|AAH06623.1| Clecsf6 protein [Mus musculus]
 Length = 262

Score = 151 bits (382), Expect = 6e-36
 Identities = 74/161 (45%), Positives = 102/161 (63%), Gaps = 5/161 (3%)

Query: 51 GKRLSELHSYHSSLTCFSEGTKVPAWGCPPASWKSFGSSCYFIS--SEEKVWSKSEQNCV 108
 G+R L S L + KV W CCP W+ FGS CY + S W+KSE+NC
 Sbjct: 105 GQRALTLESIEIDLGILAPEDKV--WSCCPKDWRFLFGSHCYLVPTVSSSASWNKSEENCS 162

Query: 109 EMGAHLVVFNTEAEQNFIIVQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGE 168
 MGAHLVV ++ EQ+FI L+ +YF+GL D G+ WQW+D+TPYE+++ FWH GE
 Sbjct: 163 RMGAHLVVIQSQEEQDFITGILDTHAAYFIGLWD-TGHRQWQWVDQTPYEESTITFWHNGE 221

Query: 169 PNHSSEQCASIVFWKPTGWGWNDVICETRRNSICEMNKIYL 209
 P+ E+CA+I++ TGWGWND+ C ++ S+C+M KI L
 Sbjct: 222 PSSGNEKCATIIYRWKTGKGWNDISCSLKQKSVQCQMKKINL 262

>gi|18028293|gb|AAL56016.1| Fc-epsilon receptor III [Homo sapiens]
 Length = 230

Score = 148 bits (373), Expect = 7e-35
 Identities = 70/137 (51%), Positives = 92/137 (67%), Gaps = 3/137 (2%)

Query: 61 HSSLTCFSEGTVK--PAWGCPPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFN 118
 H++L C + V AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V N
 Sbjct: 86 HTTLECVKKNMPVEETAWSCCPKNWKSFSNCYFISTESASWQDSEKDCARMEAHLLVIN 145

Query: 119 TEAEQNFIIVQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSSEQCAS 178
 T+ EQ+FI Q L E +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C
 Sbjct: 146 TQEEQDFIFQNLQEEESAYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPREPSDPNERCVV 205

Query: 179 IVFWK-PTGWGWNDVIC 194
 + F K P WGWNDV C
 Sbjct: 206 LNFRKSPKRWGWNDVNC 222

>gi|23397421|ref|NP_694877.1| L RIKEN cDNA 3110037K17 [Mus musculus]
 gi|22028415|gb|AAH34893.1| L RIKEN cDNA 3110037K17 [Mus musculus]
 Length = 158

Score = 147 bits (372), Expect = 1e-34
 Identities = 70/135 (51%), Positives = 94/135 (69%), Gaps = 2/135 (1%)

Query: 76 WGCCPASWKSFGSSCYFISSE-EKVWSKSEQNCVEMGAHLVVFNTEAEQNFIQQQLNESF 134
 W CCP WK FGS CYF S++ W++S++NC MGAHLVV +++ EQ+FI L+
 Sbjct: 25 WSCCPKDWPFGSYCYFTSTDLVASWNESKENCFHMGGAHLVVIHSQEEQDFITGILDGT 84

Query: 135 SYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSSEQCASIVFWKPTGWGNDVIC 194
 +YF+GLS+P G+ WQWID+TPY+ N FWH GEP+ EQC I + TGWGW+D+ C
 Sbjct: 85 AYFIGLNSNP-GDQQWQWIDQTPYDDNTTFWHKGEPSSDNEQCIVIINHRQSTGWGWSIPC 143

Query: 195 ETRRNSICEMNKIYL 209
 ++NSIC + KIYL
 Sbjct: 144 SDKQNSICHVKKIYL 158

>gi|6753442|ref|NP_036129.1| L C-type (calcium dependent, carbohydrate recognit: superfamily member 6; dendritic cell immunoreceptor [Mus musculus]

gi|6018624|emb|CAB57870.1| L dendritic cell immunoreceptor [Mus musculus]
 gi|20467064|gb|AAM22402.1| L dendritic cell immunoreceptor [Mus musculus]
 gi|26339676|dbj|BAC33509.1| L unnamed protein product [Mus musculus]
 Length = 238

Score = 147 bits (370), Expect = 1e-34
 Identities = 70/153 (45%), Positives = 99/153 (64%), Gaps = 5/153 (3%)

Query: 61 HSSLTCFSEGTVK--PAWGCPPASWKSFGSSCYFIS--SEEKVWSKSEQNCVEMGAHLVV 116
 H+ L C + + W CCP W+ FGS CY + S W+KSE+NC MGAHLVV
 Sbjct: 87 HNELNCTKSVSPMEDKVVSCCPKDWRFLFGSHCYLVPTVSSASWNKSEENCSRMGAHLVV 146

Query: 117 FNTEAEQNFIQQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSSEQC 176
 ++ EQ+FI L+ +YF+GL D G+ WQW+D+TPYE+++ FWH GEP+ E+C
 Sbjct: 147 IQSQEEQDFITGILDTHAAYFIGLWD-TGHRQWQWVDQTPYEESTITFWHNGEPSSGNEKC 205

Query: 177 ASIVFWKPTGWGNDVICETRRNSICEMNKIYL 209
 A+I++ TGWGWND+ C ++ S+C+M KI L
 Sbjct: 206 ATIIYRWKTGWGNDISCSLKQKSVQMKKINL 238

>gi|25050261|ref|XP_194289.1| L similar to C-type lectin, superfamily member 6 ; cell immunoreceptor; C-type lectin; lectin-like immunoreceptor [Mus musculus]

gi|29387373|gb|AAH49354.1| L MGC56880 protein [Mus musculus]
 Length = 245

Score = 142 bits (359), Expect = 3e-33
 Identities = 74/198 (37%), Positives = 110/198 (55%), Gaps = 9/198 (4%)

Query: 16 LSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSEGTVK-- 73
 L L LW I LL+ F V+ ++ + ++ + H+ L C + V

Subjct: 53 LLLALW---IFFLLLAILFSVALIILFQMYSDLLEEKYTLERLNHARLHCVKNHSSVED 108
 Query: 74 PAWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNES 133
 W CCP +WK F S CYF S + WSKSE+ C GAHL+V ++ EQ+FI LN
 Subjct: 109 KVWSCCPKNWKPFDSHCYFTSRDTASWSKSEEKCSLRGAHLLVIQSQEEQDFITNTLNPR 168
 Query: 134 FSYFLGLSDPQGNWWQWIDKTPYEKNVRFWHLGEPNHSSEQCASIVFWKPT--GWWND 191
 +Y++GLSDP+G+ WQW+D+TPY++N WH EP+ + E C ++ + P GWGW+
 Subjct: 169 AAYYVGLSDPKGHGQWQWDQTPYDQNATSWHSDEPSGNTEFCV-VLSYHPNVKGWGWSV 227
 Query: 192 VICETRRNSICEMNKIYL 209
 C+ ICEM ++Y+
 Subjct: 228 APCDGDHRLICEMRQLYV 245

>gi|26387827|dbj|BAC25626.1| unnamed protein product [Mus musculus]
 Length = 152

Score = 142 bits (358), Expect = 4e-33
 Identities = 67/136 (49%), Positives = 93/136 (68%), Gaps = 3/136 (2%)
 Query: 76 WGCPASWKSFGSSCYFIS--SEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNES 133
 W CCP W+ FGS CY + S W+KSE+NC MGAHLVV ++ EQ+FI L+
 Subjct: 18 WSCCPKDWRFLFGSHCYLVPTVSSASWNKSEENCSRGAHLLVIQSQEEQDFITGILDTH 77
 Query: 134 FSYFLGLSDPQGNWWQWIDKTPYEKNVRFWHLGEPNHSSEQCASIVFWKPTGWGWNDVI 193
 +YF+GL D G+ WQW+D+TPYE+++ FWH GEP+ E+CA+I++ TGWGWND+
 Subjct: 78 AAYFIGLWD-TGHRQWQWVDQTPYEESETFWHNGEPPSGNEKCATIIYRWKTGWGWNDIS 136
 Query: 194 CETRRNSICEMNKIYL 209
 C ++ S+C+M KI L
 Subjct: 137 CSLKQKSVCQMKKINL 152

>gi|7657333|ref|NP_055173.1| C-type lectin, superfamily member 9; macrophage-lectin [Homo sapiens]
 gi|5821288|dbj|BAA83755.1| macrophage C-type lectin Mincle [Homo sapiens]
 gi|12653849|gb|AAH00715.1| C-type lectin, superfamily member 9 [Homo sapiens]
 gi|37182121|gb|AAQ88863.1| CLECSF9 [Homo sapiens]
 Length = 219

Score = 140 bits (353), Expect = 2e-32
 Identities = 82/205 (40%), Positives = 118/205 (57%), Gaps = 5/205 (2%)

Query: 3 QEQQPQSTEKRGWLS-LRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYH 61
 + + Q TE+ + S + LW+VAGI I LSACFI CVVT+ + ++ +L
 Subjct: 5 KSSETQCTERGFSSQMFLWTVAGIPILFLSACFITRCVVTFRI-FQTCDEKKFQLPENF 63
 Query: 62 SSLTCFSEGKVPAWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEA 121
 + L+C++ G+ CCP +W+ F SSCYF S++ W+ S +NC MGAHLVV N++
 Subjct: 64 TELSCNYGSG-SVKNCCPLNWEYFQSSCYFFSTDITISWALSLKNCSAMGAHLVVINSQE 122
 Query: 122 EQNFIVQQLNESFSYFLGLSDPQGNWWQWIDKTPYEKNVRFWHLGEPNHSAA-EQCASI 179
 EQ F+ + + F+GLSD WQW+D TP K++ FW +GEPN+ A E CA++
 Subjct: 123 EQEFLSYKKPKMREFFIGLSDQVVEGQWQWDGTPLTKSLSFWDVGEPNNIATLEDATM 182
 Query: 180 VFWKPTGWGNDVICETRRNSICEM 204

WNDV C ICEM
 Sbjct: 183 RDSSNPRQNWNDFTCFLNYFRICEM 207

[>] >gi|34858417|ref|XP_342753.1| L similar to RIKEN cDNA 3110037K17 [Rattus norvegicus]
 Length = 237

Score = 140 bits (352), Expect = 2e-32
 Identities = 64/135 (47%), Positives = 91/135 (67%), Gaps = 2/135 (1%)

Query: 76 WGCCPASWKSFGSSCYFISSEE-KVWSKSEQNCVEMGAHLVVFNTEAEQNFIIVQLNESF 134
 W CCP WK F S+CYF S++ + W +SE+ C +GAHLVV +++ EQ+F+ + L+
 Sbjct: 104 WS CCPKDWKPFDSNCYFPSTD SVESWM ESEEKCSGIGAHLVVIHSQEEQDFLPRILDTHA 163

Query: 135 SYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGE PN HSAEQCASIVFWKPTGWGNDVIC 194
 +YF+GLSDP G+ W QW+D+TPY N FWH GEP+ EQC I + TGWGW+D C
 Sbjct: 164 AYFIGLSDP-GH RQWQWVDQTPYNGNATFWHEGE PSSDNEQC VIINHHENTGWGWS DSSC 222

Query: 195 ETRRNSICEMNKIYL 209
 ++ +C++ KIYL
 Sbjct: 223 SDKQKLVCQVKKIYL 237

[>] >gi|34858419|ref|XP_232393.2| L similar to dendritic cell immunoreceptor [Rattus norvegicus]
 Length = 767

Score = 137 bits (345), Expect = 1e-31
 Identities = 65/134 (48%), Positives = 86/134 (64%), Gaps = 4/134 (2%)

Query: 71 TKVPAWG CCPASWKSFGSSCYFISSEEK-VWSKSEQNCVEMGAHLVVFNTEAEQNFIIVQQ 129
 T+ A CC WKSFGS CYF S++ K W +S++ C MGAHL+V +++ EQ+FI
 Sbjct: 99 TEDKACSCCLKGWKSFGSYCYFTSTD SKATWDESKECSR MG AHLLVIHSQDEQDFINTI 158

Query: 130 LN ESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGE PN HSAEQCASIVFWKPTGWG 189
 LN YF+GLSD N W QWID+TPY ++V FWH GEPN+ E+C +V WGW
 Sbjct: 159 LNIGTDYFIGLSD-HSENQWQWIDQTPYNESVTFWHKGE PNNKEEKC--V VVINHRDKWG 215

Query: 190 NDVICETRRNSICE 203
 ND+ C R S+C
 Sbjct: 216 NDIPCHDRHKSVCQ 229

Score = 94.7 bits (234), Expect = 9e-19
 Identities = 41/81 (50%), Positives = 54/81 (66%), Gaps = 1/81 (1%)

Query: 123 QNFIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGE PN HSAEQCASIVFW 182
 ++FI L+ + YF GLSD QG N W QWID+TPY ++V FWH EPN+ E+C I
 Sbjct: 503 EDFINGILDTRWGYFTGLSD-QGQNQWQWIDQTPYNESVTFWHEDEPNNDYEKCVEINHH 561

Query: 183 KPTGWGNDVICETRRNSICE 203
 K GWGWND++C + SIC+
 Sbjct: 562 KDIGWGNDIVCSSEHKSICQ 582

Score = 47.0 bits (110), Expect = 2e-04

Identities = 22/33 (66%), Positives = 26/33 (78%)

Query: 41 VTYHFTYGETGKRLSELHSYHSSLTCFSEGTKV 73

VTY FT + +RLSELH+YHSSLTC S+GT V

Sbjct: 660 VTYQFTMEKPNRRLSELHTYHSSLTCCSKGTMV 692

Score = 37.7 bits (86), Expect = 0.12

Identities = 17/37 (45%), Positives = 24/37 (64%), Gaps = 1/37 (2%)

Query: 121 AEQNFIIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPY 157

A ++FI LN +YF+GL D G+ WQW+ +TPY

Sbjct: 382 AVRDFITGFLNRDAAYFIGLWD-SGHRQWQWVSQTPY 417

[>] >gi|9910162|ref|NP_064332.1| L C-type lectin, superfamily member 9 [Mus musculus]
 gi|5821286|dbj|BAA83754.1| L macrophage C-type lectin Mincle [Mus musculus]
 gi|13096844|gb|AAH03218.1| L C-type lectin, superfamily member 9 [Mus musculus]
 Length = 214

Score = 129 bits (323), Expect = 4e-29

Identities = 77/189 (40%), Positives = 110/189 (58%), Gaps = 5/189 (2%)

Query: 21 WSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSEGTKVPAWGCPP 80

W++AG SI LS CFI CVVTY + +G+ L + H L+C+SE + CCP

Sbjct: 25 WTIAGASILFLSGCFITRCVVTYR-SSQISGQNL-QPHRNIKELSCYSEASG-SVKNCCP 81

Query: 81 ASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIIVQQLNESFSYFLGL 140

+WK + SSCYF S+ WS S +NC +MGAHLVV +T+ EQ F+ + + +++GL

Sbjct: 82 LNWKHYQSSCYFFSTTLTWSSSLKNCSDMGAHLVVIDTQEEQEFLFRTPKRKEFYIGL 141

Query: 141 SDPQGNNNWQWIDKTPYEKNVRFWHLGEPEPNHS--AEQCASIVFWKPTGWGWNDVICETRR 198

+D WQW+D TP+ +++ FW GEPN+ E CA+I + WND+ C

Sbjct: 142 TDQVVEGQWQVDDTPFTESLSFWDAGEPNNIVLVEDCATIRDSSNSRKNWNDIPCFYSM 201

Query: 199 NSICEMNKI 207

ICEM +I

Sbjct: 202 PWICEMPEI 210

[>] >gi|25392184|pir||JC7595 scavenger receptor with C-type lectin type I - human
 gi|13365515|dbj|BAB39147.1| L scavenger receptor with C-type lectin type I [Homo
 Length = 742

Score = 95.5 bits (236), Expect = 5e-19

Identities = 49/146 (33%), Positives = 78/146 (53%), Gaps = 14/146 (9%)

Query: 68 SEGTKVPAWGCPPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIIV 127

+E T P CP WK+F CY+ S E++++ ++ C + +HLV NT EQ +I

Sbjct: 596 NEPTPAPEDNSCPPHWKNFTDKCYYFSVEKEIFEDAHLFCEDKSSHGVINTREEQQWIK 655

Query: 128 QQLNESFSYFLGLSDPQGNNNWQWIDKT-PYEKNVRFWHLGEPENH-----SAEQCASIV 180

+Q+ S+++GL+D + N W+W+D T P KN W G+P++ E CA ++

Sbjct: 656 KQMVGRESHWIGLTD SERENE NEWKWL DGTSPDYKN---WKAGQPDNWGHGHGP GEDCAGLI 712

Query: 181 FWKPTGKGNDVICETRRNSICEMNK 206
 + WND CE N ICE ++
 Sbjct: 713 Y----AGQWNDFQCEDVNNFICEKDR 734

[>] >gi|38174510|gb|AAH60789.1| L Collectin sub-family member 12, isoform I [Homo sa Length = 742

Score = 95.5 bits (236), Expect = 5e-19
 Identities = 49/146 (33%), Positives = 78/146 (53%), Gaps = 14/146 (9%)

Query: 68 SEGTKVPAWGCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFI 127
 +E T P CP WK+F CY+ S E++++ ++ C + +HLV NT EQ +I
 Sbjct: 596 NEPTPAPEDNSCPPHWKNFTDKCYYFSVEKEIFEDAQLFCEDKSSHGVFINTREEQQWIK 655

Query: 128 QQLNESFSYFLGLSDPQGNNNWQWIDKT-PYEKNVRFWHLGEPNH-----SAEQCASIV 180
 +Q+ S+++GL+D + N W+W+D T P KN W G+P++ E CA ++
 Sbjct: 656 KQMVGRESHWIGLTDSERENEWKWLGTSPDYKN--WKAGQPDNWGHGHGPAGEDCAGLI 712

Query: 181 FWKPTGKGNDVICETRRNSICEMNK 206
 + WND CE N ICE ++
 Sbjct: 713 Y----AGQWNDFQCEDVNNFICEKDR 734

[>] >gi|34858415|ref|XP_342752.1| L similar to C-type (calcium dependent, carbohydrate domain) lectin, superfamily member 6; dendritic cell immunoreceptor; C-type lectin [Rattus norvegicus]
 Length = 126

Score = 95.5 bits (236), Expect = 6e-19
 Identities = 43/118 (36%), Positives = 71/118 (60%), Gaps = 3/118 (2%)

Query: 94 SSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFI VQQLNESFSYFLGLSDPQGNNNWQWID 153
 + + WS SE+ C GAHL+V +++ EQ+FI LN Y++GLSD +G+ WQW+D
 Sbjct: 10 TGDSASWSDSEEKCShRGAHLLVIHSQEEQDFITDTLNPRAHYYVGLSDTEHGKQWVD 69

Query: 154 KTPYEKNVRFWHLGEPNHSAEQCASIVFWKPT--GWGNDVICETRRNSICEMNKIYL 209
 +TP+ +N WH EP+ + C ++ + P GWGW+ C+ +C+M ++Y+
 Sbjct: 70 QTPFNQNATSWHADEPSGNKGFCV-VLSYHPNLKGWGSVAPCDGYHRLVCKMRQLYV 126

[>] >gi|27356791|gb|AAL89528.1| putative CD209L1 protein [Hylobates lar]
 Length = 399

Score = 95.1 bits (235), Expect = 8e-19
 Identities = 51/128 (39%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFI VQQLNESFSY-F 137
 CP W F +CYFIS+ ++ W S C E+GA LVV + EQNF+ Q + S + +
 Sbjct: 268 CPKDWTFFQGNCYFISNSQRNWHDSTACREVGAQLVVIKSAEEQNFLQLQSSRSNRFAW 327

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHSA-EQCASIVFWKPTGKGNDVICE 195
 +GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C
 Sbjct: 328 MGLSDLNQEQTWQWDGSPLSSSFQRYWNSGEPNNSGDEDCAEF-----SGSGWNDNRCN 382

Query: 196 TRRNSICE 203

IC+

Sbjct: 383 VDNYWICK 390

[>gi|18641360|ref|NP_569057.1| L collectin sub-family member 12 isoform I; scavenger C-type lectin; collectin placenta 1; scavenger receptor class A, member 4 [Homo sapiens]

gi|17026101|dbj|BAB72147.1| L collectin placenta 1 [Homo sapiens]
Length = 742

Score = 94.7 bits (234), Expect = 8e-19
Identities = 49/146 (33%), Positives = 78/146 (53%), Gaps = 14/146 (9%)

Query: 68 SEGTKVPAWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIV 127
+E T P CP WK+F CY+ S E++++ ++ C + +HLV NT EQ +I
Sbjct: 596 NEPTPAPEDNGCPPHWKNFTDKCYYFSVEKEIFEDAFLFCEDKSSHVLVFINTREEQQWIK 655

Query: 128 QQLNESFSYFLGLSDPQGNNNWQWIDKT-PYEKNVRFWHLGEPNH-----SAEQCASIV 180
+Q+ S++GL+D + N W+W+D T P KN W G+P++ E CA ++
Sbjct: 656 KQMVGRESHWIGLTDSERENEWKLDGTSPDYKN---WKAGQPDNWGHGHGPGEDCAGLI 712

Query: 181 FWKPTGKGNDVICETRRNSICEMNK 206
+ WND CE N ICE ++
Sbjct: 713 Y----AGQWNDFQCEDVNNFICEKDR 734

[>gi|27356800|gb|AAL89529.1| putative CD209L1 protein [Hylobates syndactylus]
Length = 422

Score = 94.7 bits (234), Expect = 9e-19
Identities = 50/128 (39%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSY-F 137
CP W F +CYF+S+ ++ W S C E+GA LVV + EQNF+ Q + S ++
Sbjct: 291 CPKDWTFFQGNACYFMSNSQRNWHDSVTACQEVAQLVVIKSAEEQNFLQLQTSRSNRFSW 350

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHSA-EQCASIVFWKPTGKGNDVICE 195
+GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C
Sbjct: 351 MGLSDLNQEGTWQVWDGSPLSSSFQRYWNSGEPNNSGDEDCAEF----SGSGWNDNRCN 405

Query: 196 TRRNSICE 203
IC+
Sbjct: 406 VDNYWICK 413

[>gi|27356809|gb|AAL89530.1| putative CD209L1 protein [Hylobates concolor]
Length = 399

Score = 94.7 bits (234), Expect = 1e-18
Identities = 51/128 (39%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSY-F 137
CP W F +CYFIS+ ++ W S C E+GA LVV + EQNF+ Q + S ++
Sbjct: 268 CPKDWTFFQGNACYFISNSQRNWHDSVTACQEVAQLVVIKSAEEQNFLQLQSSRSNRFTW 327

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHSA-EQCASIVFWKPTGKGNDVICE 195

+GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C
 Sbjct: 328 MGLSDLNQEGTWQWVDGSPLSSSFQRYWNSGEPNNSGDEDCAEF-----SGSGWNDNRNCN 382

Query: 196 TRRNSICE 203
 IC+
 Sbjct: 383 VDNYWICK 390

[>gi|12084795|gb|AAG13815.2| L probable mannose binding C-type lectin DC-SIGNR [gi|15383606|gb|AAK91859.1| mDC-SIGN2 type I isoform [Homo sapiens]
 gi|24416563|gb|AAH38851.1| L CD209L protein [Homo sapiens]
 Length = 399

Score = 93.6 bits (231), Expect = 2e-18
 Identities = 50/128 (39%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIHQQLNESFSY-F 137
 CP W F +CYF+S+ ++ W S C E+ A LVV T EQNF+ Q + S + +
 Sbjct: 268 CPKDWTFFQGNCYFMSNSQRNWHDSVTACQEVRALVVIKTAEEQNFLQLQTSRSNRFSW 327

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHSA-EQCASIVFWKPTGWWNDVICE 195
 +GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C+
 Sbjct: 328 MGLSDLNQEGTWQWVDGSPLSPSFQRYWNSGEPNNSGDEDCAEF-----SGSGWNDNRCD 382

Query: 196 TRRNSICE 203
 IC+
 Sbjct: 383 VDNYWICK 390

[>gi|20149606|ref|NP_055072.2| L CD209 antigen-like; putative type II membrane protein [Homo sapiens]
 gi|13383470|gb|AAK20998.1| L L-SIGN [Homo sapiens]
 Length = 376

Score = 92.8 bits (229), Expect = 3e-18
 Identities = 50/128 (39%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIHQQLNESFSY-F 137
 CP W F +CYF+S+ ++ W S C E+ A LVV T EQNF+ Q + S + +
 Sbjct: 245 CPKDWTFFQGNCYFMSNSQRNWHDSVTACQEVRALVVIKTAEEQNFLQLQTSRSNRFSW 304

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHSA-EQCASIVFWKPTGWWNDVICE 195
 +GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C+
 Sbjct: 305 MGLSDLNQEGTWQWVDGSPLSPSFQRYWNSGEPNNSGDEDCAEF-----SGSGWNDNRCD 359

Query: 196 TRRNSICE 203
 IC+
 Sbjct: 360 VDNYWICK 367

[>gi|19584340|emb|CAD28466.1| L hypothetical protein [Homo sapiens]
 Length = 417

Score = 92.4 bits (228), Expect = 4e-18
 Identities = 49/146 (33%), Positives = 78/146 (53%), Gaps = 14/146 (9%)

Query: 68 SEGTKVPAWGCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIV 127
 +E T P CP WK+F CY+ S E++++ ++ C + +HLV NT EQ +I
 Sbjct: 271 NEPTPAPEDNGCPPHWKNFTDKCYYFSVEKEIFEDAQLFCEDKSSHGVFINTREEQQWIK 330

Query: 128 QQLNESFSYFLGLSDPQGNNNWQWIDKT-PYEKNVRFWHLGEPNH-----SAEQCASIV 180
 +Q+ S+++GL+D + N W+W+D T P KN W G+P++ E CA ++
 Sbjct: 331 KQMVGRESHWIGLTDSERENEWKWLDGTSPDYKN---WKAGQPDNWGHGHGPGEDCAGLI 387

Query: 181 FWKPTGWGWNNDVICETRRNSICEMNK 206
 + WND CE N ICE ++
 Sbjct: 388 Y----AGQWNDFQCEDVNNFICEKDR 409

[>gi|27356856|gb|AAL89536.1] putative CD209L1 protein [Pan troglodytes]
 Length = 445

Score = 92.0 bits (227), Expect = 6e-18
 Identities = 49/128 (38%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSY-F 137
 CP W F +CYF+S+ ++ W S C E+ A LVV + EQNF+ Q + S ++
 Sbjct: 314 CPKDWTFFQGNCYFMSNSQRNWHNSVTACREVRAQLVVIKSAEEQNFLQLQTSRSNRFSW 373

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHSA-EQCASIVFWKPTGWGWNNDVICE 195
 +GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C+
 Sbjct: 374 MGLSDLNQEQTWQVWDGSPLSPSFQRYWNSGEPNNSGNEDCAEF-----SGSGWNDNRCD 428

Query: 196 TRRNSICE 203
 IC+
 Sbjct: 429 IDNYWICK 436

[>gi|15383614|gb|AAK91863.1] [L] sDC-SIGN2 type I isoform [Homo sapiens]
 Length = 332

Score = 91.3 bits (225), Expect = 9e-18
 Identities = 50/128 (39%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSY-F 137
 CP W F +CYF+S+ ++ W S C E+ A LVV T EQNF+ Q + S ++
 Sbjct: 201 CPKDWTFFQGNCYFMSNSQRNWHDSVTACQEVRAQLVVIKTAEEQNFLQLQTSRSNRFSW 260

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHSA-EQCASIVFWKPTGWGWNNDVICE 195
 +GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C+
 Sbjct: 261 MGLSDLNQEQTWQVWDGSPLSPSFQRYWNSGEPNNSGNEDCAEF-----SGSGWNDNRCD 315

Query: 196 TRRNSICE 203
 IC+
 Sbjct: 316 VDNYWICK 323

[>gi|18157520|dbj|BAB83835.1] supported by GENSCAN and partially homologous to t1
 domain [Oryzias latipes]
 Length = 236

Score = 91.3 bits (225), Expect = 9e-18
 Identities = 53/132 (40%), Positives = 69/132 (52%), Gaps = 9/132 (6%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIQQQLNESF--SY 136
 CP +W F SSCYFIS++ K W S+ C GAHL + +T EQ F+ L + +Y
 Sbjct: 101 CPTNWHLFNSSCYFISTQMKPWRDSQTYCQRQGAHLAIHTAEEQTFLWDLLPRAHWNAY 160

Query: 137 FLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEP-NHSAEQCASI----VFWKPTGWGWND 191
 + G+SD Q + W+W+D T EK+ FW GEP NH EC I V + W D
 Sbjct: 161 WFGISDRQKEDEWKWVDGTSVEKS--FWEEGEPNNHINEDCGYIVKTQVLERVAIRSWYD 218

Query: 192 VICETRRNSICE 203
 CE ICE
 Sbjct: 219 APCEMSIFICE 230

[>gi|27356845|gb|AAL89534.1] putative CD209L1 protein [Gorilla gorilla]
 Length = 376

Score = 91.3 bits (225), Expect = 9e-18
 Identities = 49/128 (38%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIQQQLNESFSY-F 137
 CP W F +CYF+S+ ++ W S C E+ A LVV + EQNF+ Q + S + +
 Sbjct: 245 CPKDWTFFQGNCYFMSNSQRNWHNSVTACQEVRALVVIKSAEEQNFLQLQTSRSNRFSW 304

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHSA-EQCASIVFWKPTGWGWNDVICE 195
 +GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C+
 Sbjct: 305 MGLSDLNQEGTWQWVDGSPLSPSFQRYWNSGEPPNNSGNEDCAEF----SGSGWNDNRCD 359

Query: 196 TRRNSICE 203
 IC+
 Sbjct: 360 VDNYWICK 367

[>gi|34870124|ref|XP_344065.1] L similar to SIGNR3 [Rattus norvegicus]
 Length = 212

Score = 90.9 bits (224), Expect = 1e-17
 Identities = 48/127 (37%), Positives = 67/127 (52%), Gaps = 7/127 (5%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIQQQLNESFSYFL 138
 CP W F SCYF S ++ W S C E+GA LV+ T+ EQ F+ Q ++
 Sbjct: 81 CPRDWTFFNGSCYFFSKSQRNWHNSITACKELGAQLVIVETDEEQTFLQQTSKTRGPTWM 140

Query: 139 GLSDPQGNNNWQWIDKTPYEKN-VRFWHLGEPNHSA-EQCASIVFWKPTGWGWNDVICET 196
 GLSD W W+D +P + ++W+ GEPN+ E CA +G GWND+ C+T
 Sbjct: 141 GLSDMHNEATWHWVDGSPLSPSFAQYWRNGEPNNVGDEDCAEF----SGDWNDLRCDT 195

Query: 197 RRNSICE 203
 R IC+
 Sbjct: 196 RIFWICK 202

[>gi|27356883|gb|AAL89539.1] putative CD209 protein [Hylobates syndactylus]
 Length = 381

Score = 90.5 bits (223), Expect = 2e-17
 Identities = 49/130 (37%), Positives = 73/130 (56%), Gaps = 8/130 (6%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIIVQQLNESFSY-F 137
 CP W F +CYF+S+ ++ W S C E+GA LVV + EQNF+ Q + S + +
 Sbjct: 233 CPWEWTFFQGNCYFMSNSQRDWQDSVTACQEVTAGAQLVVIKSAEEQNFLQLQSSRSNRF 292

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNVR-FWHLGEPNHSAEQ-CASIVFWKPTGWGWNNDVICE 195
 +GLSD WQW+D +P + + +W+ GEPN+ E+ CA +G GWND C
 Sbjct: 293 MGLSDVNQEGTWQWVDGSPLSPSFKHYNRGEPPNNIGEEDCAEF-----SGNGWNDDKCN 347

Query: 196 TRRNSICEMN 205
 + IC+M+
 Sbjct: 348 HAKFWICKMS 357

[>] >gi|27356854|gb|AAL89535.1| putative CD209L1 protein [Pan troglodytes]
 Length = 445

Score = 90.5 bits (223), Expect = 2e-17
 Identities = 48/128 (37%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIIVQQLNESFSY-F 137
 CP W F +CYF+S+ ++ W S C E+ A LVV + EQNF+ Q + S + +
 Sbjct: 314 CPKDWTFFQGNCYFMSNSQRNWHSVTACREVRAQLVVIKSAEEQNFLQLQTSRSNRFSW 373

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNVR-FWHLGEPNHSA-EQCASIVFWKPTGWGWNNDVICE 195
 +GLSD WQW+D +P + + +W+ GEPN+S E CA +G GWND C+
 Sbjct: 374 MGLSDLNQEGTWQWVDGSPLSPSFQXYWNSGEPNNSGNEDCAEF-----SGSGWNNDNRCD 428

Query: 196 TRRNSICE 203
 IC+
 Sbjct: 429 IDNYWICK 436

[>] >gi|12084797|gb|AAG13848.2| [L] probable mannose binding C-type lectin DC-SIGNR [I]
 Length = 399

Score = 90.1 bits (222), Expect = 2e-17
 Identities = 47/127 (37%), Positives = 70/127 (55%), Gaps = 6/127 (4%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIIVQQLNESFSY-F 137
 CP W F +CYF+S+ ++ W S C E+ A LVV T EQNF+ Q + S + +
 Sbjct: 268 CPKDWTFFQGNCYFMSNSQRNWHDSTACQEVTAGAQLVVIKTAEEQNFLQLQTSRSNRFSW 327

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHSAEQCASIVFWKPTGWGWNNDVICET 196
 +GLSD WQW+D +P + R+W+ GEPN+S + + + +G GWND C+
 Sbjct: 328 MGLSDLNQEGTWQWVDGSPLSPSFQRYWNSGEPNNSGNEDXA---EFSGSGWNNDNRCDV 383

Query: 197 RRNSICE 203
 IC+
 Sbjct: 384 DNYWICK 390

[>] >gi|27356874|gb|AAL89538.1| putative CD209 protein [Hylobates lar]

Length = 450

Score = 89.4 bits (220), Expect = 4e-17
Identities = 48/128 (37%), Positives = 71/128 (55%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIQQQLNESFSY-F 137
CP W F +CYF+S+ ++ W S C E+GA LVV + EQNF+ Q + S + +
Sbjct: 302 CPWEWTFFQGNCYFMSNSQRDWHDSVTACQEVAQLVVIKSAEEQNFLQLQSSRSNRF AW 361

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNVR-FWHLGEPNHSSEQ-CASIVFWKPTGWGWNDVICE 195
+GLSD WQW+D P + + +W+ GEPN+ E+ CA +G GWND C
Sbjct: 362 MGLSDLNQEGTWQWDGSPLSPSFHQYWNRGEPPNNVGEEDCAEF-----SGNGWNDDKCN 416

Query: 196 TRRNSICE 203
+ IC+
Sbjct: 417 LAKFWICK 424

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Jan 26, 2004 1:24 AM
Number of letters in database: 530,365,172
Number of sequences in database: 1,612,710

Lambda K H
0.319 0.132 0.446

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 46,303,767
Number of Sequences: 1612710
Number of extensions: 1858764
Number of successful extensions: 4428
Number of sequences better than 10.0: 250
Number of HSP's better than 10.0 without gapping: 136
Number of HSP's successfully gapped in prelim test: 114
Number of HSP's that attempted gapping in prelim test: 4087
Number of HSP's gapped (non-prelim): 291
length of query: 209
length of database: 530,365,172
effective HSP length: 119
effective length of query: 90
effective length of database: 338,452,682
effective search space: 30460741380
effective search space used: 30460741380
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)

X3: 64 (24.7 bits)
S1: 41 (21.8 bits)
S2: 70 (31.6 bits)